Nickol
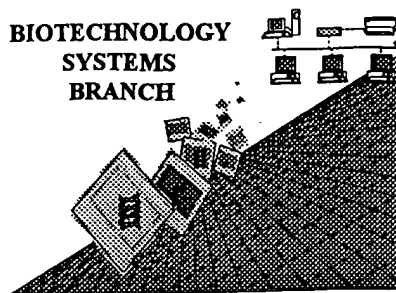
RAW SEQUENCE LISTING ERROR REPORT

P#8

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/451,739A_

Source: _1642_

Date Processed by STIC: _7/12/2000_

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TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

G. Nickol

RAW SEQUENCE LISTING   DATE: 07/12/2000
PATENT APPLICATION: US/09/451,739A   TIME: 15:56:26

Input Set : A:\lud-5615.txt
Output Set: N:\CRF3\07122000\I451739A.raw

```
 1 <110> APPLICANT: Jager, Dirk
 2           Scanlan, Matthew
 3           Gure, Ali
 4           Jager, Elke
 5           Knuth, Alexander
 6           Old, Lloyd
 7           Chen, Yao-tseng
 9 <120> TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigens,
10           the Antigens per se, and Uses Thereof
12 <130> FILE REFERENCE: LUD 5615
14 <140> CURRENT APPLICATION NUMBER: 09/451,739A
16 <141> CURRENT FILING DATE: 1999-11-30
18 <160> NUMBER OF SEQ ID NOS: 19
```

ERRORED SEQUENCES

```
527 <210> SEQ ID NO: 16
528 <211> LENGTH: 528      512 shown (next page)
529 <212> TYPE: PRT
530 <213> ORGANISM: Homo sapiens
531 <220> FEATURE:
532 <400> SEQUENCE: 16
533 Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln
534 1               5                   10                  15
536 Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala
537             20                  25                  30
539 Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn
540         35                  40                  45
542 Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln
543     50                  55                  60
545 Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr
546 65              70                  75                  80
548 Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His Gln Lys Glu
549             85                  90                  95
551 Ile Asp Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asp Asn Asp Gly
552         100                 105                 110
554 Phe Leu Lys Ala Pro Cys Arg Met Lys Val Ser Ile Pro Thr Lys Ala
555         115                 120                 125
557 Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys
558     130                 135                 140
560 Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn
561 145                 150                 155                 160
563 Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln Met
564             165                 170                 175
566 Phe Pro Ser Glu Ser Lys Gln Lys Lys Val Glu Glu Asn Ser Trp Asp
567             180                 185                 190
```

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```
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          569 Ser Glu Ser Leu Arg Glu Thr Val Ser Gln Lys Asp. Val Cys Val Pro
          570         195                 200                 205
          572 Lys Ala Thr His Gln Lys Glu Met Asp Lys Ile Ser Gly Lys Leu Glu
          573         210                 215                 220
          575 Asp Ser Thr Ser Leu Ser Lys Ile Leu Asp Thr Val His Ser Cys Glu
          576 225                 230                 235                 240
          578 Arg Ala Arg Glu Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys
E--> 579                   260 245                 265 250                 270 255
          581 Met Glu Gln Met Lys Lys Lys Phe Cys Val Leu Lys Lys Lys Leu Ser
E--> 582             275 260                 280 265                 285 270
          584 Glu Ala Lys Glu Ile Lys Ser Gln Leu Glu Asn Gln Lys Val Lys Trp
E--> 585             290 275                 295 280                 300 285
          587 Glu Gln Glu Leu Cys Ser Val Arg Leu Thr Leu Asn Gln Glu Glu Glu
E--> 588 305                 310                 315                 320
          590 Lys Arg Arg Asn Ala Asp Ile Leu Asn Glu Lys Ile Arg Glu Glu Leu
E--> 591                 325                 330                 335
          593 Gly Arg Ile Glu Glu Gln His Arg Lys Glu Leu Glu Val Lys Gln Gln
E--> 594                 340                 345                 350
          596 Leu Glu Gln Ala Leu Arg Ile Gln Asp Ile Glu Leu Lys Ser Val Glu
E--> 597         355                 360                 365
          599 Ser Asn Leu Asn Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu
E--> 600         370                 375                 380
          602 Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu
E--> 603 385                 390                 395                 400
          605 Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr
E--> 606                 405                 410                 415
          608 Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln Met
E--> 609                 420                 425                 430
          611 Thr Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr
E--> 612         435                 440                 445
          614 Ser Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr Ser
E--> 615         450                 455                 460
          617 Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu
E--> 618 465                 470                 475                 480
          620 Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile
E--> 621                 485                 490                 495
          623 Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp
E--> 624                 500                 505                 510
          626 Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Asp Ile
E--> 627         515                 520                 525
```

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY   DATE: 07/12/2000
PATENT APPLICATION: US/09/451,739A   TIME: 15:56:27

Input Set : A:\lud-5615.txt
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```
L:25  M:283 W: Missing Blank Line separator, <220> field identifier
L:28  M:283 W: Missing Blank Line separator, <400> field identifier
L:35  M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:35  M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:86  M:283 W: Missing Blank Line separator, <220> field identifier
L:87  M:283 W: Missing Blank Line separator, <400> field identifier
L:133 M:283 W: Missing Blank Line separator, <220> field identifier
L:134 M:283 W: Missing Blank Line separator, <400> field identifier
L:166 M:283 W: Missing Blank Line separator, <220> field identifier
L:167 M:283 W: Missing Blank Line separator, <400> field identifier
L:203 M:283 W: Missing Blank Line separator, <220> field identifier
L:204 M:283 W: Missing Blank Line separator, <400> field identifier
L:264 M:283 W: Missing Blank Line separator, <220> field identifier
L:265 M:283 W: Missing Blank Line separator, <400> field identifier
L:313 M:283 W: Missing Blank Line separator, <220> field identifier
L:314 M:283 W: Missing Blank Line separator, <400> field identifier
L:365 M:283 W: Missing Blank Line separator, <220> field identifier
L:368 M:283 W: Missing Blank Line separator, <400> field identifier
L:391 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:391 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
L:400 M:283 W: Missing Blank Line separator, <220> field identifier
L:401 M:283 W: Missing Blank Line separator, <400> field identifier
L:409 M:283 W: Missing Blank Line separator, <220> field identifier
L:410 M:283 W: Missing Blank Line separator, <400> field identifier
L:418 M:283 W: Missing Blank Line separator, <220> field identifier
L:419 M:283 W: Missing Blank Line separator, <400> field identifier
L:427 M:283 W: Missing Blank Line separator, <220> field identifier
L:428 M:283 W: Missing Blank Line separator, <400> field identifier
L:436 M:283 W: Missing Blank Line separator, <220> field identifier
L:437 M:283 W: Missing Blank Line separator, <400> field identifier
L:445 M:283 W: Missing Blank Line separator, <220> field identifier
L:446 M:283 W: Missing Blank Line separator, <400> field identifier
L:454 M:283 W: Missing Blank Line separator, <220> field identifier
L:457 M:283 W: Missing Blank Line separator, <400> field identifier
L:512 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:512 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
L:516 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:516 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
L:520 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:520 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
L:522 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:522 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
L:524 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:524 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
L:531 M:283 W: Missing Blank Line separator, <220> field identifier
L:532 M:283 W: Missing Blank Line separator, <400> field identifier
L:579 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:582 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
```

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PATENT APPLICATION: US/09/451,739A   TIME: 15:56:27

Input Set : A:\lud-5615.txt
Output Set: N:\CRF3\07122000\I451739A.raw

```
L:585 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:588 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:591 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:594 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:597 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:600 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:603 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:606 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:609 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:612 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:615 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:618 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:621 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:624 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:627 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:627 M:252 E: No. of Seq. differs, <211>LENGTH:Input:528 Found:512 SEQ:16
L:634 M:283 W: Missing Blank Line separator, <220> field identifier
L:635 M:283 W: Missing Blank Line separator, <400> field identifier
L:643 M:283 W: Missing Blank Line separator, <220> field identifier
L:644 M:283 W: Missing Blank Line separator, <400> field identifier
L:652 M:283 W: Missing Blank Line separator, <220> field identifier
L:653 M:283 W: Missing Blank Line separator, <400> field identifier
```